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FIGURE 1A

-28	AGTATTGTTGTCGTGTTTGCCCTTGTAAGGCGGTCATCCCTCAAGTGATCACTTAGTCAA	31
-80		-40
-20		-1
		20
32	GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC	91
-8		11
		M N T S H L L A L L L
40		80
		60
92	CCAAATCTCCACAAGGTGAAACAGAAAGCAACCCCTGGGCAACCCATACAACTTCTCT	151
12	P K S P Q G E N R S K P L G T P Y N F S	31
100		120
		140
152	GAACATTGCCAGGATTCCCGTGGACGTGATGGTCTTTCATCGTCACTTCCTACAGCATGAG	211
32	E H C Q D S V D V M V F I V T S Y S I E	51
160		180
		200
212	ACTGTCGTGGGGTCCCTGGGTAACCTCTGCCTGATGTGTGACTGTGAGGCAGAAAGGAG	271
52	T V V G V L G N L C L M C V T V R Q K E	71



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FIGURE 1B

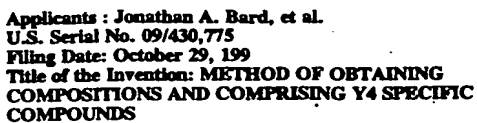
272	AAAGCCAAAGTGACCAACCTGCTTATCGCCAAACCTGGCCCTTCTCTGACTTCCTCATGTGC	220	240	260	331
72	K A N V T N L L I A N L A F S D F L M C				91
280		300	320		
332	CTCCTCTGCCAGCCGCTGACCGCCGCTACACCATCATGGACTACTGGATCTTTGGAGAG				391
92	L L C Q P L T A V Y T I M D Y W I F G E				111
340		360	380		
392	ACCCTCTGCAAGATGTCGGCCCTTCATCCAGTCCAGTGCGTGACGGTCTCCATCCTCTCG				451
112	T L C K M S A F I Q C M S V T V S I L S				131
400		420	440		
452	CTCGTCTCGTGGCCCTGGAGAGGCATCAGCTCATCAACCCAAACAGGCTGGAAGCCC				511
132	L V L V A L E R H Q L I I N P T G W K P				151
460		480	500		
512	AGCATCTCACAGGCCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCCTGTGCTCCTCC				571
152	S I S Q A Y L G I V L I W V I A C V L S				171



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FIGURE 1C

	520	540	560	
572	CTGCCCTTCCTGGCCAAACAGCATCCTGGAGAAATGTCTTCCACAAGAACCACTCCAAGGCT			631
172	L P F L A N S I L E N V F H K N H S K A			191
	580	600	620	
632	CTGGAGTTCCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGGCTCACCACCGC			691
192	L E F L A D K V V C T E S W P L A H H R			211
	640	660	680	
692	ACCATCTACACCACTTCCTGGCTCCTCTTCCAGTACTGCCCTCCCACTGGGCTTCATCCTG			751
212	T I Y T T F L L L F Q Y C L P L G F I L			231
	700	720	740	
752	GTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCGCGGTGTTTCAACAAGGC			811
232	V C Y A R I Y R R L Q R Q R V F H K G			251
	760	780	800	
812	ACCTACAGCTTGGGAGCTGGGCACATGAAGCAGGTCAATGTGCTGCTGGTGGTGGTG			871
252	T Y S L R A G H M K Q V N V V L V V M V			271



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FIGURE 1D

872	GTGGCCTTTGCGGTGCTCTGGCTGCCTCTGCA	820	840	860	931
272	V A F A V L W L P L H V F N S L E D W H				291
		880	900	920	
932	CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGTGCTTGCC				991
292	H E A I P I C H G N L I F L V C H L L A				311
		940	960	980	
992	ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTCTCTCAACACCAACTTCAAGAAG				1051
312	M A S T C V N P F I Y G F L N T N F K K				331
		1000	1020	1040	
11052	GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCTGGAGGAGTCGGAGCAT				1111
332	E I K A L V L T C Q Q S A P L E E S E H				351
		1060	1080	1100	
11112	CTGCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG				1171
352	L P L S T V H T E V S K G S L R L S G R				371



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FIGURE 1E

1172	TCCAATCCCATTTAAACCAGGTCTAGGTCTTCTCCCTGCCCATGTCCCTTGCCAGGCTCTTC	1160	1231
372	S N P I *		375
1180		1200	
1232	CACTTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCAGCCAGCATTCCTGGCTTTCTG	1220	1291



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FIGURE 2B

hp25a human Y1 rat Y1 mouse Y1	201	CTESWPLAHH RTIYTTFILL FQYCLPLGFI CFDQFPDSH RLSYTTLLLV LQYFGPLCFI CFDKFPDSH RLSYTTLLLV LQYFGPLCFI CFDKFPDSH RLSYTTLLLV LQYFGPLCFI	V	LVCYARIYRR LQYQGRVFKH FICYFKIYIR LKRRNNMMDK FICYFKIYIR LKRRNNMMDK FICYFKIYIR LKRRNNMMDK	250
hp25a human Y1 rat Y1 mouse Y1	251	GTYS.LRAGH MKQNVVIVV MVVAFVAVLWL MRDNKYRSSE TKRINIMLLS IVVAFVAVCWL IRDSKYRSSE TKRINVMLLS IVVAFVAVCWL IRDSKYRSSE TKRINIMLLS IVVAFVAVCWL	VI	PLHVFNSLED WHHEAIPICH PLTIFNTVFD WNHQIIATCN PLTIFNTVFD WNHQIIATCN PLTIFNTVFD WNHQIIATCN	300
hp25a human Y1 rat Y1 mouse Y1	301	GNIIFLVCHL LAMASTCVNP FIYGFNLNTNF HNLLFLLCHL TAMISTCVNP IFYGFNLKNF HNLLFLLCHL TAMISTCVNP IFYGFNLKNF HNLLFLLCHL TAMISTCVNP IFYGFNLKNF	VII	KKEIKALVLT CQQSAPLEES QRDLQFFNF CDFRSRDDY QRDLQFFNF CDFRSRDDY QRDLQFFNF CDFRSRDDY	350



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FIGURE 2C

hp25a	351	EHLPLSTVHT	EVSKGSLRLS	GRSNPI*...	388
human Y1		ETIAMSTMHT	DVSKTSLKQA	SPVAFKKINN	NDDNEKI*	
rat Y1		ETIAMSTMHT	DVSKTSLKQA	SPVAFKKISM	N.DNEKI*	
mouse Y1		ETIAMSTMHT	DVSKTSLKQA	SPVAFKKISM	N.DNEKV*	



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FIGURE 3A

-170 -150 -130

ATAGCTCTCAAGCCATAAGATATAAGTAGCTAAGAATTGTCTCCCTCTCCCTGTCCCTTG

-110 -90 -70

TTCTTACCTGGTTCCATTTTACATGCCTGGACCTTTGAGTTCCATTTGTTTGTGTTTGCAG

-50 -30 -10

GCTACACTCAGAAGTGGGCCCTTTAGTCTTGAAGTTCCTGGTCTTCTCACACCCACCATG

M

10 30 50

AATACCTCTCATCTCATGGCCTCCCTTTCTCCGGCATTTCCTACAAGGTAAGAATGGGACC

N T S H L M A S L S P A F L Q G K N G T

70 90 110

AACCCACTGGATTCCCTCTATAATCTCTCTGACGGCTGCCAGGATTCCGGCAGATCTGTTG

N P L D S L Y N L S D G C Q D S A D L L

130 150 170

GCCTTCATCATCACCACCTACAGCGTTGAGACCGTCTTGGGGTCTTAGGAAACCTCTGC

A F I I T T Y S V E T V L G V L G N L C

190 210 230

TTGATATTTGTGACCACAAGGCAAAAGGAAAAGTCCAATGTGACCAACCTACTCATTGCC

L I F V T T R Q K E K S N V T N L L I A



TTTGTGTCCTGGTCCTCGGATCACCACCGCCTCATCTACACCACCTTTCTGCTGCTCTTC
F V S W S S D H H R L I Y T T F L L L F



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FIGURE 3C

670	690	710
CAATACTGCGTCCCTCTGGCCTTCATCCTGGTCTGCTACATGCGTATCTATCAGCGCCTG		
Q Y C V P L A F I L V C Y M R I Y Q R L		
730	750	770
CAGAGGCAGAGGCGTGCGTTCCACACGCACACTTGCAGCTCACGAGTGGGGCAGATGAAG		
Q R Q R R A F H T H T C S S R V G Q M K		
790	810	830
CGGATCAATGGCATGCTCATGGCAATGGTGACTGCCTTTGCAGTTCTCTGGCTGCCCCTG		
R I N G M L M A M V T A F A V L W L P L		
850	870	890
CATGTGTTCAACACTCTGGAGGACTGGTACCAGGAAGCCATCCCTGCTTGCCATGGCAAC		
H V F N T L E D W Y Q E A I P A C H G N		
910	930	950
CTCATCTTCTTGATGTGCCACCTGTTTGCCATGGCTTCCACCTGTGTCAACCCTTTCATC		
L I F L M C H L F A M A S T C V N P F I		
970	990	1010
TATGGCTTTCTCAACATCAACTTCAAGAAGGACATCAAGGCTCTGGTTCTGACCTGCCGT		
Y G F L N I N F K K D I K A L V L T C R		
1030	1050	1070
TGCAGGCCACCTCAAGGGGAGCCTGAGCCTCTGCCCCTGTCCACTGTGCACACGGACCTC		
C R P P Q G E P E P L P L S T V H T D L		



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FIGURE 3D

1090	1110	1130
TCCAAGGATCTATGAGGATGGGTAGCAAGTCTAACGTCACTAGTCATGTCTAGGCTCT		
S K G S M R M G S K S N V M *		
1150	1170	1190
TCCGCCATTCTTCGACACACCCCTTTCACCTGAGCTAAGTAGACACAAATGCAAGCTGTG		
1210	1230	1250
GTATCATCCTGCCATTCTGTGTCCTTTGGGGCCAGACAGCGCGCAAGAGACTTGAAGCTT		



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FIGURE 4

1		50
Y4rat	MNTSHLMASL SPAFLQGKNG TNPLDSLYNL SDGCQDSADL LAFIITTYSV	
Y4hum	MNTSHLLALL LPKSPQGENR SKPLGTPYNF SEHCQDSVDV MVFIVTSYSI	
51		100
	I	II
Y4rat	ETVLGVLGNL CLIFVTTRQK EKSNTVNLLI ANLAFSDFLM CLICQPLTVT	
Y4hum	ETVVGVLGNL CLMCVTVRQK EKANVTNLLI ANLAFSDFLM CLLCQPLTAV	
101		150
	III	
Y4rat	YTIMDYWIPG EVLCKMLTFI QCMSVTVSIL SLVLVALERH QLIINPTGWK	
Y4hum	YTIMDYWIPG ETLCKMSAFI QCMSVTVSIL SLVLVALERH QLIINPTGWK	
151		200
	IV	
Y4rat	PSISQAYLGI VVIWFISCFL SLPFLANSIL NDLFHYNHSHK VVEFLEDKVV	
Y4hum	PSISQAYLGI VLIWVIACVL SLPFLANSIL ENVFHKNHSHK ALEFLADKVV	
201		250
	V	
Y4rat	CFVSWSSDHH RLIYTTFLLL FQYCVPLAFI LVCYMRIYQR LQRQRRAFHT	
Y4hum	CTESWPLAHH RTIYTTFLLL FQYCLPLGFI LVCYARIYRR LQRQGRVFHK	
251		300
	VI	
Y4rat	HTCSSRVGQM KRINGMLMAM VTAPAVLWLP LHVFNLTLEDW YQEAIPACHG	
Y4hum	GTYSLRAGHM KQNVVVLVVM VVAPAVLWLP LHVFNLSLEDW HHEAIPICHG	
301		350
	VII	
Y4rat	NLIFLMCHLF AMASTCVNPF IYGFLNINFK KDIKALVLTC RCRPPQGEPE	
Y4hum	NLIFLVCHLL AMASTCVNPF IYGFLNTNFK KEIKALVLTC QQSAPLEESE	